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# SEQUENCE LISTING

<110> Jackson, Stephen P  
Critchlow, Susan E

<120> Assays, agents, therapy and diagnosis relating to  
modulation of cellular DNA repair activity

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<140> US 09/341,505

<141> 1999-07-12

<150> PCT/GB98/00095

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<150> GB 9713131.2

<151> 1997-06-20

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<170> PatentIn Ver. 2.1

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ttgcgagggc ttaatthttt gaagtttatt taatactatc ctacatatgt acattaaata 3240
cttcgtaac gtttatcaat aagagtggaa gatgcgcaat tatattcaaa agattggcca 3300
gtcaattaac ttaaggaaaa aat 3323

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<210> 7
<211> 5
<212> PRT
<213> Saccharomyces cerevisiae

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<400> 7
Ala Glu Ile Ser Val
  1                      5

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<210> 8
<211> 6
<212> PRT
<213> Saccharomyces cerevisiae

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<400> 8
Leu Arg Thr Leu Tyr Met
  1                      5

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```

<210> 9
<211> 11
<212> PRT
<213> Saccharomyces cerevisiae

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<400> 9
His Cys Asp Ile Asn Arg Lys Ile Arg Arg Val
  1                      5                      10

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<210> 10  
 <211> 43  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 10  
 Ile Asn Asn Ile Gly Phe Ile Thr Tyr Val Val Cys Ala Val Leu Glu  
           1                  5                  10                  15  
 Leu Arg Ser Phe Ser Ile Pro Tyr Phe Leu Leu Phe Ser Phe Phe Leu  
                   20                  25                  30  
 Leu Phe Phe Ser Phe Tyr Leu Leu Ser Pro Tyr  
           35                  40

<210> 11  
 <211> 5  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 11  
 Ile Phe Lys Gln Ile  
           1                  5

<210> 12  
 <211> 7  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 12  
 Lys Asn Pro Leu Asn Ile Cys  
           1                  5

<210> 13  
 <211> 6  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 13  
 Tyr Val Glu Asn Lys Tyr  
           1                  5

<210> 14  
 <211> 959  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 14  
 Asn Lys Asn Leu Glu Leu Lys Glu Ile Val Thr Asp Tyr Leu Gly Met  
           1                  5                  10                  15

Ile Ser Ala Leu Asp Ser Ile Pro Glu Pro Gln Asn Phe Ala Pro Ser  
 20 25 30  
 Pro Asp Phe Lys Trp Leu Cys Glu Glu Leu Phe Val Lys Ile His Glu  
 35 40 45  
 Val Gln Ile Asn Gly Thr Ala Gly Thr Gly Lys Ser Arg Ser Phe Lys  
 50 55 60  
 Tyr Tyr Glu Ile Ile Ser Asn Phe Val Glu Met Trp Arg Lys Thr Val  
 65 70 75 80  
 Gly Asn Asn Ile Tyr Pro Ala Leu Val Leu Ala Leu Pro Tyr Arg Asp  
 85 90 95  
 Arg Arg Ile Tyr Asn Ile Lys Asp Tyr Val Leu Ile Arg Thr Ile Cys  
 100 105 110  
 Ser Tyr Leu Lys Leu Pro Lys Asn Ser Ala Thr Glu Gln Arg Leu Lys  
 115 120 125  
 Asp Trp Lys Gln Arg Val Gly Lys Gly Gly Asn Leu Ser Ser Leu Leu  
 130 135 140  
 Val Glu Glu Ile Ala Lys Arg Arg Ala Glu Pro Ser Ser Lys Ala Ile  
 145 150 155 160  
 Thr Ile Asp Asn Val Asn His Tyr Leu Asp Ser Leu Ser Gly Asp Arg  
 165 170 175  
 Phe Ala Ser Gly Arg Gly Phe Lys Ser Leu Val Lys Ser Lys Pro Phe  
 180 185 190  
 Leu His Cys Val Glu Asn Met Ser Phe Val Glu Leu Lys Tyr Phe Phe  
 195 200 205  
 Asp Ile Val Leu Lys Asn Arg Val Ile Gly Gly Gln Glu His Lys Leu  
 210 215 220  
 Leu Asn Cys Trp His Pro Asp Ala Gln Asp Tyr Leu Ser Val Ile Ser  
 225 230 235 240  
 Asp Leu Lys Val Val Thr Ser Lys Leu Tyr Asp Pro Lys Val Arg Leu  
 245 250 255  
 Lys Asp Asp Asp Leu Ser Ile Lys Val Gly Phe Ala Phe Ala Pro Gln  
 260 265 270  
 Leu Ala Lys Lys Val Asn Leu Ser Tyr Glu Lys Ile Cys Arg Thr Leu  
 275 280 285  
 His Asp Asp Phe Leu Val Glu Glu Lys Met Asp Gly Glu Arg Ile Gln  
 290 295 300  
 Val His Tyr Met Asn Tyr Gly Glu Ser Ile Lys Phe Phe Ser Arg Arg  
 305 310 315 320

Gly Ile Asp Tyr Thr Tyr Leu Tyr Gly Ala Ser Leu Ser Ser Gly Thr  
 325 330 335  
 Ile Ser Gln His Leu Arg Phe Thr Asp Ser Val Lys Glu Cys Val Leu  
 340 345 350  
 Asp Gly Glu Met Val Thr Phe Asp Ala Lys Arg Arg Val Ile Leu Pro  
 355 360 365  
 Phe Gly Leu Val Lys Gly Ser Ala Lys Glu Ala Leu Ser Phe Asn Ser  
 370 375 380  
 Ile Asn Asn Val Asp Phe His Pro Leu Tyr Met Val Phe Asp Leu Leu  
 385 390 395 400  
 Tyr Leu Asn Gly Thr Ser Leu Thr Pro Leu Pro Leu His Gln Arg Lys  
 405 410 415  
 Gln Tyr Leu Asn Ser Ile Leu Ser Pro Leu Lys Asn Ile Val Glu Ile  
 420 425 430  
 Val Arg Ser Ser Arg Cys Tyr Gly Val Glu Ser Ile Lys Lys Ser Leu  
 435 440 445  
 Glu Val Ala Ile Ser Leu Gly Ser Glu Gly Val Val Leu Lys Tyr Tyr  
 450 455 460  
 Asn Ser Ser Tyr Asn Val Ala Ser Arg Asn Asn Asn Trp Ile Lys Val  
 465 470 475 480  
 Lys Pro Glu Tyr Leu Glu Glu Phe Gly Glu Asn Leu Asp Leu Ile Val  
 485 490 495  
 Ile Gly Arg Asp Ser Gly Lys Lys Asp Ser Phe Met Leu Gly Leu Leu  
 500 505 510  
 Val Leu Asp Glu Glu Glu Tyr Lys Lys His Gln Gly Asp Ser Ser Glu  
 515 520 525  
 Ile Val Asp His Ser Ser Gln Glu Lys His Ile Gln Asn Ser Arg Arg  
 530 535 540  
 Arg Val Lys Lys Ile Leu Ser Phe Cys Ser Ile Ala Asn Gly Ile Ser  
 545 550 555 560  
 Gln Glu Glu Phe Lys Glu Ile Asp Arg Lys Thr Arg Gly His Trp Lys  
 565 570 575  
 Arg Thr Ser Glu Val Ala Pro Pro Ala Ser Ile Leu Glu Phe Gly Ser  
 580 585 590  
 Lys Ile Pro Ala Glu Trp Ile Asp Pro Ser Glu Ser Ile Val Leu Glu  
 595 600 605  
 Ile Lys Ser Arg Ser Leu Asp Asn Thr Glu Thr Asn Met Gln Lys Tyr  
 610 615 620

Ala	Thr	Asn	Cys	Thr	Leu	Tyr	Gly	Gly	Tyr	Cys	Lys	Arg	Ile	Arg	Tyr	625	630	635	640
Asp	Lys	Glu	Trp	Thr	Asp	Cys	Tyr	Thr	Leu	Asn	Asp	Leu	Tyr	Glu	Ser	645	650	655	
Arg	Thr	Val	Lys	Ser	Asn	Pro	Ser	Tyr	Gln	Ala	Glu	Arg	Ser	Gln	Leu	660	665	670	
Gly	Leu	Ile	Arg	Lys	Lys	Arg	Lys	Arg	Val	Leu	Ile	Ser	Asp	Ser	Phe	675	680	685	
His	Gln	Asn	Arg	Lys	Gln	Leu	Pro	Ile	Ser	Asn	Ile	Phe	Ala	Gly	Leu	690	695	700	
Leu	Phe	Tyr	Val	Leu	Ser	Asp	Tyr	Val	Thr	Glu	Asp	Thr	Gly	Ile	Arg	705	710	715	720
Ile	Thr	Arg	Ala	Glu	Leu	Glu	Lys	Thr	Ile	Val	Glu	His	Gly	Gly	Lys	725	730	735	
Leu	Ile	Tyr	Asn	Val	Ile	Leu	Lys	Arg	His	Ser	Ile	Gly	Asp	Val	Arg	740	745	750	
Leu	Ile	Ser	Cys	Lys	Thr	Thr	Thr	Glu	Cys	Lys	Ala	Leu	Ile	Asp	Arg	755	760	765	
Gly	Tyr	Asp	Ile	Leu	His	Pro	Asn	Trp	Val	Leu	Asp	Cys	Ile	Ala	Tyr	770	775	780	
Lys	Arg	Leu	Ile	Leu	Ile	Glu	Pro	Asn	Tyr	Cys	Phe	Asn	Val	Ser	Gln	785	790	795	800
Lys	Met	Arg	Ala	Val	Ala	Glu	Lys	Arg	Val	Asp	Cys	Leu	Gly	Asp	Ser	805	810	815	
Phe	Glu	Asn	Asp	Ile	Ser	Glu	Thr	Lys	Leu	Ser	Ser	Leu	Tyr	Lys	Ser	820	825	830	
Gln	Leu	Ser	Leu	Pro	Pro	Met	Gly	Glu	Leu	Glu	Ile	Asp	Ser	Glu	Val	835	840	845	
Arg	Arg	Phe	Pro	Leu	Phe	Leu	Phe	Ser	Asn	Arg	Ile	Ala	Tyr	Val	Pro	850	855	860	
Arg	Arg	Lys	Ile	Ser	Thr	Glu	Asp	Asp	Ile	Ile	Glu	Met	Lys	Ile	Lys	865	870	875	880
Leu	Phe	Gly	Gly	Lys	Ile	Thr	Asp	Gln	Gln	Ser	Leu	Cys	Asn	Leu	Ile	885	890	895	
Ile	Ile	Pro	Tyr	Thr	Asp	Pro	Ile	Leu	Arg	Lys	Asp	Cys	Met	Asn	Glu	900	905	910	
Val	His	Glu	Lys	Ile	Lys	Glu	Gln	Ile	Lys	Ala	Ser	Asp	Thr	Ile	Pro	915	920	925	

15

Lys Ile Ala Arg Val Val Ala Pro Glu Trp Val Asp His Ser Ile Asn  
930 935 940

Glu Asn Cys Gln Val Pro Glu Glu Asp Phe Pro Val Val Asn Tyr  
945 950 955

<210> 15

<211> 13

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 15

Trp Cys Val Leu Arg Arg Leu Asn Phe Leu Lys Phe Ile  
1 5 10

<210> 16

<211> 7

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 16

Tyr Tyr Pro Thr Tyr Val His  
1 5

<210> 17

<211> 19

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 17

Arg Leu Ser Ile Arg Val Glu Asp Ala Gln Leu Tyr Ser Lys Asp Trp  
1 5 10 15

Pro Val Asn

<210> 18

<211> 4

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 18

Leu Lys Glu Lys  
1